

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: THE GENERAL HOSPITAL CORPORATION
FRUIT STREET
BOSTON, MA 02114
UNITED STATES OF AMERICA

APPLICANT/INVENTOR: de la Monte, Suzanne
Wands, Jack R.

(ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
- (B) STREET: 1100 New York Ave., Suite 600
- (C) CITY: Washington
- (D) STATE: DC
- (E) COUNTRY: USA
- (F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: To be assigned
- (B) FILING DATE: Herewith
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/038,908
- (B) FILING DATE: 26-FEB-1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Esmond, Robert W.
- (B) REGISTRATION NUMBER: 32,893
- (C) REFERENCE/DOCKET NUMBER: 0609.437PC01

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 202-371-2600
- (B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 15..1139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTGAG ATG GAG TTT TCG CTC TTG CCC AGG CTG GAG TGC Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys 1 5 10	50
AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser 15 20 25	98
GAT TCT CCT GCC TCA GCC TCC CCA GTA GCT GGG ATT ACA GGC ATG TGC Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys 30 35 40	146
ACC CAC GCT CGG CTA ATT TTG TAT TTT TTA GTA GAG ATG GAG TTT Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe 45 50 55 60	194
CTC CAT GTT GGT CAG GCT GGT CTC GAA CTC CCG ACC TCA GAT GAT CCC Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro 65 70 75	242
TCC GTC TCG GCC TCC CAA AGT GCT AGA TAC AGG ACT GGC CAC CAT GCC Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala 80 85 90	290
CGG CTC TGC CTG GCT AAT TTT TGT AGA AAC AGG GTT TCA CTG ATG Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met 95 100 105	338
TGC CCA AGC TGG TCT CCT GAG CTC AAG CAG TCC ACC TGC CTC AGC CTC Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu 110 115 120	386
CCA AAG TGC TGG GAT TAC AGG CGT GCA GCC GTG CCT GGC CTT TTT ATT Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile 125 130 135 140	434
TTA TTT TTA AGA CAC AGG TGT CCC ACT CTT ACC CAG GAT GAA GTG Leu Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val 145 150 155	482
CAG TGG TGT GAT CAC AGC TCA CTG CAG CCT TCA ACT CCT GAG ATC AAG Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys	530

	160	165	170	
CAT CCT CCT GCC TCA GCC TCC CAA GTA GCT GGG ACC AAA GAC ATG CAC His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His	175	180	185	578
CAC TAC ACC TGG CTA ATT TTT ATT TTT ATT TTT AAT TTT TTG AGA CAG His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln	190	195	200	626
AGT CTC AAC TCT GTC ACC CAG GCT GGA GTG CAG TGG CGC AAT CTT GGC Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly	205	210	215	674
TCA CTG CAA CCT CTG CCT CCC GGG TTC AAG TTA TTC TCC TGC CCC AGC Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser	225	230	235	722
CTC CTG AGT AGC TGG GAC TAC AGG CGC CCA CCA CGC CTA GCT AAT TTT Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe	240	245	250	770
TTT GTA TTT TTA GTA GAG ATG GGG TTC ACC ATG TTC GCC AGG TTG ATC Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile	255	260	265	818
TTG ATC TCT GGA CCT TGT GAT CTG CCT GCC TCG GCC TCC CAA AGT GCT Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala	270	275	280	866
GGG ATT ACA GGC GTG AGC CAC CAC GCC CGG CTT ATT TTT AAT TTT TGT Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys	285	290	295	914
TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp	305	310	315	962
CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe	320	325	330	1010
TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro	335	340	345	1058
CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr	350	355	360	1106
TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg	365	370	375	1159
TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA				1219

AAATATGTAG	CAATGGGGGG	TCTTGCTATG	TTGCCCGAGGC	TGGTCTCAA	AACTTCTGGCTT	1279
CATGCAATCC	TTCCAAATGA	GCCACAAACAC	CCAGGCCAGTC	ACATTTTTA	AACAGTTACA	1339
TCTTTATTTT	AGTATACTAG	AAAGTAATA	CAC AATAAACATG	TCAAACCTGC	AAATTCA	1399
GTAACAGAGT	TCTTTATAA	CTTTAAACA	AAGCTTTAGA	GCA		1442

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: protein
 - xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: ,

Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile
 1 5 10 15

Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala
 20 25 30

Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
 35 40 45

Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
 50 55 60

Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
 65 70 75 80

Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu
 85 90 95

Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
 100 105 110

Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
 115 120 125

Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
 130 135 140

Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp
 145 150 155 160

His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
 165 170 175

Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
 180 185 190

Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
195 200 205

Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
210 215 220

Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
225 230 235 240

Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
245 250 255

Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
260 265 270

Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
275 280 285

Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
290 295 300

Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
305 310 315 320

Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
325 330 335

Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
340 345 350

Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp
355 360 365

Ser Gln Thr Pro Asp Leu Arg
370 375

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT 60
CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120
AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTTTAGTA 180

GAGATGGAGT TTAACCTCCAT GTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC 240
TCCCGTCTCG GCCTGCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC 300
TGCCTGGCTA ATTTTGTTGG TAGAACAGG GTTCACTGA TGTTGCCAA GCTGGTCTCC 360
TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GGCAGTCAGCC 420
GTGCCTGGCC TTTTATTTT ATTTTTTTA AGACACAGGT GTACCACTCT TACCCAGGAT 480
GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTCAA CTCCTGAGAT CAAGCAATCC 540
TCCTGCCTCA GCCTCCCAAG TAGCTGGAC CAAAGACATG CACCACTACA CCTGGTAATT 600
TTTATTTTTA TTTTAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC 660
AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCCCTCCGG GTTCAAGTTA TTCTCCTGCC 720
CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTTGTAT 780
TTTTAGTAGA GATGGGGTTT CACCATGTTG GCCAGGTTGA TCTTGATCTC TTGACCTTGT 840
GATCTGCCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTCGTGACT CCACGCCGGC 900
CTATTTTAA TTTTGTGG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC 960
AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCGGG TCAAGCGATT CTCCTGTCTC 1020
AGCCTCCAA GCAGCTGGGA TTACGGGACC TGCACCAACAC CCCGCTAATT TTTGTATTT 1080
CATTAGAGGC GGGTTTACCA TATTGTCAG GCTGGGTCTC AAACCTCTGA CCTCAGGTGA 1140
CCCACCTGCC TCAGCCTTCC AAAGTGTGG GATTACAGGC GTGAGGCCACC TCACCCAGCC 1200
GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260
TCAAAATTCT GGCTTCAGTC AATCCTTCCA AATGAGGCCAC AACACCCAGC CAGTCACATT 1320
TTTAAACAG TTACATCTT ATTGAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA 1380
C 1381

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1418 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTTTTTT GAGATGGAGT	TTTCGCTCTT	GTTGCCAGG	CTGGAGTGCA	ATGGCGCAAT	60	
CTCAGCTCAC	CGCAACCTCC	GCCTCCCGGG	TTCAAGCGAT	TCTCCTGCCT	CAGCCTCCCC	120
AGTAGGCTGG	GATTACAGGC	ATGTGCACCA	CGCTCGGCTA	ATTTGTATT	TTTTTTAGT	180
AGAGATGGAG	TTCTCCATG	TTGGTCAGGC	TGGTCTCGAA	CTCCGACCTC	AGATGATCCT	240
CCCGTCTCGG	CCTCCCAAAG	TGCTAGATAAC	AGGACTGAGC	ACCATGCCCG	GCCTCTGCCT	300
GGCTAATT	TTGTGGTAGAA	ACAGGGTTTC	ACTGATGTGC	CCAAGCTGGT	CTCCTGAGCT	360
CAAGCAGTCC	ACCTGCCTCA	GCCTCCAAA	GTGCTGGGAT	TACAGGCGTG	CAGCCGTGCC	420
TGGCCTTTT	ATTTTATT	TTTAAGACA	CAGGTGTCCC	ACTCTTACCC	AGGATGAAGT	480
GCAGTGGTGT	GATCACAGCT	CACTGCAGCC	TTCAACTCTG	AGATCAAGCA	TCCTCCTGCC	540
TCAGCCTCCC	AAAGTAGCTG	GGACCAAAGA	CATGCACCAC	TACACCTGGC	TAATTTTAT	600
TTTTATT	AAATTGGA	GACAGAGTCT	CAACTCTGTC	ACCCAGGCTG	GAGTGCAGTG	660
GCGCAATCTT	GGCTCACTGC	AACCTCTGCC	TCCCGGGTTC	AAGTTATTCT	CCTGCCAG	720
CCTCCTGAGT	AGCTGGGACT	ACAGGCGCCC	ACCACGCCTA	GCTAATT	TTGTATT	780
AGTAGAGATG	GGGTTTCACC	ATGTTGCCA	GGTTGATGCT	AGATCTCTG	ACCTGTGAT	840
CTGCCTGCC	CGGCCTCCC	AAGTGCTGGG	ATTACAGGAC	GTGACGCCA	CCGCCGGCC	900
TATTTTAAT	TTTGTTTGT	TTGAAATGGA	ATCTCACTCT	GTTACCCAGG	CTGGAGTGCA	960
ATGGCCAAAT	CTCGGCTCAC	TGCAACCTCT	GCCTCCCGGG	CTCAAGCGAT	TCTCCTGTCT	1020
CAGCCTCCC	AGCAGCTGGG	ATTACGGCA	CCTGCACCAC	ACCCCGCTAA	TTTTGTATT	1080
TTCATTAGAG	GCGGGTTTC	ACCATATTG	TCAGGCTGGT	CTCAAACCTCC	TGACCTCAGG	1140
TGACCCACCT	GCCTCAGCCT	TCCAAAGTGC	TGGGATTACA	GGCGTGACGC	CTCACCCAGC	1200
CGGCTAATT	AGATAAAAAAA	ATATGTAGCA	ATGGGGGGTC	TTGCTATGTT	GCCCAGGCTG	1260
GTCTCAAAC	TCTGGCTTCA	TGCAATCCTT	CCAAATGAGC	CACAACACCC	AGCCAGTCAC	1320
ATTTTAAAC	AGTTACATCT	TTATTAGT	ATACTAGAAA	GTGATACGAT	AACATGGCGG	1380
AACCTGAAA	TTCGAGTAGT	ACAGAGTCTT	TTATAACT			1418

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTCCCCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGCAG ATCACAAAGGT CCAG

24

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

-60-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCAC TT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14